CLAIMS

WHAT IS CLAIMED IS:

1. A method of correcting oligo probes, the method comprising:

measuring signals from each oligo probe during multiple hybridizations within a linear range;

calculating a correction coefficient for each oligo probe by requiring its signal average to be equal to a constant; and

determining an uncertainty coefficient for each oligo probe.

2. The method of claim 1 and further comprising calculating an average and standard deviation for signals observed on each probe.

3. The method of claim 2 wherein the correction coefficients are calculated based on requiring its signal average to be equal to a constant.

4. The method of claim 3 wherein the uncertainty coefficient is based on a ratio of the average to the standard deviation.

5. The method of claim 1 and further comprising deciding whether to redesign or disregard a probe having an uncertainty coefficient greater than a predetermined value.

6. The method of claim 5 wherein the predetermined value is approximately 1.0.

7. A system for correcting oligo probes, the method comprising:

means for measuring signals from each oligo probe during multiple hybridizations within a linear range;

means for calculating a correction coefficient for each oligo probe by requiring its signal average to be equal to a constant; and

means for determining an uncertainty coefficient for each oligo probe.

8. A method of obtaining correction coefficients for probes, the method comprising:

determining a dynamic range for gDNA binding;

measuring signals from each probe during multiple hybridizations with gDNA within the linear range;

normalizing the signal intensities from different hybridizations;

calculating a correction coefficient for each probe; and

calculating an uncertainty coefficient for each probe.

9. The method of claim 8 and further comprising calculating an average and standard deviation for signals observed on each probe.

10. The method of claim 9 wherein the correction coefficients are calculated based on requiring its signal average to be equal to a constant.

11. The method of claim 10 wherein the uncertainty coefficient is based on a ratio of the average to the standard deviation.

12. The method of claim 8 and further comprising deciding whether to redesign or disregard a probe having an uncertainty coefficient greater than a predetermined value.

13. The method of claim 12 wherein the predetermined value is approximately 1.0.

14. A method of obtaining correction coefficients for probes, the method comprising:

determining a dynamic range for gDNA binding;

measuring signals from each probe during multiple hybridizations with gDNA within the linear range;

normalizing the signal intensities from different hybridizations;

calculating a correction coefficient for each probe; and

calculating an uncertainty coefficient for each probe.

15. A computer implemented method of using correction coefficients for oligo probes, the method comprising:

calculating a corrected signal for a probe using a corresponding correction coefficient;

calculating a weighting factor for a probe;

calculating an expression level for a gene as a function of the weighting factor; and

calculating an uncertainty of the gene expression.

16. The method of claim 15 and further comprising converting the corrected signal to a number of copies per cell.

17. The method of claim 16 and further comprising converting measurements of other genes to the number of copies per cell.

18. The method of claim 16 wherein the measurements of other genes are corrected based on a known number of copies per cell for a corrected signal.

19. The method of claim 15 wherein the weighting factor for a probe is proportional to an uncertainty coefficient associated with each probe.

20. The method of claim 19 wherein the weighting factor for a probe is equal to the uncertainty coefficient for the probe divided by the sum of uncertainty coefficients for all the probes for the gene.

21. The method of claim 15 wherein the expression level for a gene is the sum of weight times the corresponding corrected signal for the probes used to detect the gene divided by the number of probes used to detect the gene.

22. The method of claim 15 wherein the uncertainty of the gene expression level is based on the sum of the uncertainty coefficient for a probe times the corresponding corrected signal divided by the number of probes used to detect the gene.

23. The method of claim 15 wherein each probe has an associated uncertainty coefficient, and wherein the probe with the highest uncertainty is discarded prior to using the correction coefficients.

24. The method of claim 15 and further comprising making a call for the gene based on the uncertainty of the gene expression level.

25. The method of claim 24 wherein making a call further comprises:
subtracting a background from the average intensities of probes;
normalizing probe intensities globally;
applying the correction coefficient to each probe; and
determining a call based upon a Z-score for the gene.

26. The method of claim 24 wherein the call is made by a person.

27. A computer readable medium having instructions for causing a computer to perform a method of using correction coefficients for oligo probes, the method comprising:
calculating a corrected signal for a probe using a corresponding correction coefficient;
calculating a weighting factor for a probe;
calculating an expression level for a gene as a function of the weighting factor; and
calculating an uncertainty of the gene expression.

28. A system that uses correction coefficients for oligo probes, the system comprising:
a module that calculates a corrected signal for a probe using a corresponding correction coefficient;
a module that calculates a weighting factor for a probe;
a module that calculates an expression level for a gene as a function of the weighting factor; and

a module that calculates an uncertainty of the gene expression.